C2 Cont.

predetermined to form a hydrophobic core, and into one or more sub segment sequences which are not predetermined to form a hydrophobic core.

REMARKS

Initially, Applicant thanks the Examiner for returning a duly initialed copy of the Forms PTO-1449 with the Office Action, indicating consideration of the documents cited in the Information Disclosure Statements filed June 25, 2002, and indicating consideration of pages 11, 12, 21, 22 and 249 of Branden et al. Applicants note that the form PTO-1449 included with the Office Action is a copy of the form returned with the October 3, 2001 Office Action, and although it states on the right hand side that Branden et al. was "not considered", the left hand column contains the Examiner's initials and the date 6/28/02 and the Examiner has stated in the current Office Action that Branden et al. has been considered.

Applicant also thanks the Examiner for withdrawing the previous rejections under 35 U.S.C. §§ 102, 103 and 112, second paragraph.

Reconsideration and withdrawal of the rejections of record are respectfully requested.

Summary of Status of Amendments and Office Action

In the present amendment, claims 1 and 3 are amended and claims 2 and 12 are canceled. Therefore, claims 1, 3-11 and 13-20 are pending in the application with claim 1 being independent.

Claims 11-20 are rejected under 35 U.S.C. § 101 as being directed to non-statutory subject matter.

Claims 1-20 are rejected under 35 U.S.C. § 102(b) as being anticipated by Eisenberg et al. (U.S. Patent No. 5,436,580) (incorrectly identified in the Office Action as U.S. Patent No. 5,436,1995).

Response to § 101 Rejection

Claims 11-20 are rejected under 35 U.S.C. § 101 as being directed to non-statutory material. The Office Action asserts that the database is analogous to a music CD, and does not extend the functionality of the computer. The Office Action further asserts that the database merely contains a collection of data which is used by a computer program which accomplishes the method of claim 1.

In response, Applicant notes that the use of the database claimed in claims 11-20 extends the functionality of a computer by allowing the method of claim 1 to be performed. The use of a database containing the sequence information, including the side chain environmental data, allows for the method of claim 1 to work more efficiently and accurately than previous methods of predicting the three dimensional structure of query proteins. Thus, Applicant respectfully submits that the claimed database in fact does extend the functionality of a computer by allowing the performance of the method of claim 1.

Applicant therefore, respectfully requests that the Examiner withdraw the rejection of claim 11 under 35 U.S.C. § 101.

Response to § 102(b) Rejection

Claims 1-20 are rejected under 35 U.S.C. § 102(a) as being anticipated by Eisenberg et al. (U.S. Patent No. 5,436,580). The Office Action asserts that Eisenberg teaches a method of identifying a protein's sequence that fold into a predetermined 3-D structure. It is asserted that the method compares an environmental string of the predetermined proteins' residues stored in a database. The Office Action also asserts that the method assigns various environmental classes for each residue of the template/query protein, such as buried core structure, fraction of side chains covered by polar atoms and recites the degrees of burial of the residue. It is asserted that the method disclosed by Eisenberg generates a 3-D structure profile for each of the environmental strings of proteins, creating a 3D-1D score and compares the query protein to the predetermined proteins in the database, resulting in a Z-score which expresses the degree of match.

In response, Applicant notes that the specification discusses Eisenberg's basic method at page 3, first full paragraph. The method disclosed in Eisenberg et al. (U.S. Patent No. 5,436,580) differs only slightly from that discussed in the specification, but still suffers from the same problems noted with the 3D-1D method discussed in the last paragraph of page 3. Because there are few proteins which have the same number of amino acids, or which have the same secondary structure, or which have the same lengths of loops, many problems have been noted with the use of this method. Among the problems noted are the introduction of gaps which reduces the reliability of the predicted structure, the lack of guidance as to how to correspond sequences which have low homology and the inability to advance the predictability by improving the values of the parameters.

By contrast, Applicant has discovered that these problems can be overcome by using at least two partial sequences when matching the query protein to a reference protein sequence. This method gives a more accurate prediction of the scaffold of the query protein because it does not rely upon matching to only one protein with known tertiary structure, and therefore, gaps between the sequences are minimized. Eisenberg does not disclose the use of at least two partial sequences as disclosed and claimed in Applicant's method. Thus, Eisenberg does not, and cannot anticipate Applicant's claimed invention. Therefore, in view of the above Applicant respectfully requests that the Examiner reconsider and withdraw the rejection of claims 1-20 under 35 U.S.C. § 102(b).

CONCLUSION

For the reasons advanced above, Applicant respectfully submits that all pending claims patentably define Applicant's invention. Allowance of the application with an early mailing date of the Notices of Allowance and Allowability is therefore respectfully requested.

Should the Examiner have any further comments or questions, the Examiner is invited to contact the undersigned at the below-listed telephone number.

Respectfully submitted,
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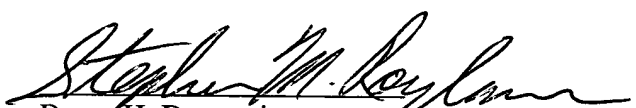

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APPENDIX

MARKED UP COPY OF AMENDED CLAIMS

1. (Twice Amended) A method of predicting a scaffold of a protein comprising a query sequence, wherein said method uses a database which contains environmental information on the side chain of each amino acid residue contained in the amino acid sequence of each reference protein whose three-dimensional structure is predetermined, and wherein said method comprises: conducting matching based on the environmental information of each amino acid residue of each reference protein and hydrophobicity or hydrophilicity property of the side chain of each amino acid residue of the query sequence, choosing at least one protein as a template protein from the reference proteins that has high similarity in three-dimensional structure to the protein comprising the query sequence, and predicting the scaffold of the protein comprising a query sequence, wherein the amino acid sequence of each of the reference proteins is divided into two or more segment sequences comprising two or more continuous amino acid residues based on the characteristics of the three-dimensional structure of the reference protein.

3. (Twice Amended) The method according to claim [2] 1, wherein the amino acid sequence of each of the reference proteins is divided into one or more core segment sequences which are predetermined to form a hydrophobic core, and into one or more sub segment sequences which are not predetermined to form a hydrophobic core.